

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/612,914DATE: 10/13/2000  
TIME: 05:29:57

INPUT SET: S36003.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Hanna, Nabil  
Newman, Roland A.  
Reff, Mitchell E.

(ii) TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
Therapy

(iii) NUMBER OF SEQUENCES: 59

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
(B) STREET: 699 Prince Street  
(C) CITY: Alexandria  
(D) STATE: VA  
(E) COUNTRY: USA  
(F) ZIP: 22314-3187

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/612,914  
(B) FILING DATE: 10-JUL-2000  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/523,894  
(B) FILING DATE: 06-SEP-1995

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Teskin, Robin L.  
(B) REGISTRATION NUMBER: 35,030  
(C) REFERENCE/DOCKET NUMBER: 012712-165

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 703-836-6620  
(B) TELEFAX: 703-836-2021

ENTERED

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47 (2) INFORMATION FOR SEQ ID NO:1:
48
49 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 420 base pairs
51 (B) TYPE: nucleic acid
52 (C) STRANDEDNESS: single
53 (D) TOPOLOGY: linear
54
55 (ii) MOLECULE TYPE: DNA (genomic)
56
57 (vi) ORIGINAL SOURCE:
58 (A) ORGANISM: Monkey
59
60 (viii) POSITION IN GENOME:
61 (A) CHROMOSOME/SEGMENT: light variable domain of CE9.1
62
63 (ix) FEATURE:
64 (A) NAME/KEY: CDS
65 (B) LOCATION: 4..420
66
67 (ix) FEATURE:
68 (A) NAME/KEY: mat_peptide
69 (B) LOCATION: 61..420
70
71
72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
73
74 GAC ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA 48
75 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg
76 -19 -15 -10 -5
77
78 TGG GTC TTG TCC CAG GTG CAG CTG CAG GAG GCG GGC CCA GGA CTG GTG 96
79 Trp Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val
80 1 5 10
81
82 AAG CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC 144
83 Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser
84 15 20 25
85
86 ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA GGG AAG 192
87 Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys
88 30 35 40
89
90 GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT 240
91 Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn
92 45 50 55 60
93
94 TAC AAT CCC TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC 288
95 Tyr Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser
96 65 70 75
97
98 AAG AAC CTC TTC TCC CTG AAA CTG AGG TCT GTG ACC GCC GCG GAC ACC 336
99 Lys Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr

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100                               80                               85                               90
101
102 GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT CAC TGG TTA      384
103 Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu
104           95                               100                               105
105
106 TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC      420
107 Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser
108     110                               115                               120
109
110

```

## (2) INFORMATION FOR SEQ ID NO:2:

### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

121
122 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
123 -19           -15           -10           -5
124
125 Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val Lys
126           1           5           10
127
128 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile
129     15           20           25
130
131 Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly
132   30           35           40           45
133
134 Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr
135           50           55           60
136
137 Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys
138           65           70           75
139
140 Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala
141           80           85           90
142
143 Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu
144     95           100           105
145
146 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser
147   110           115           120
148

```

## (2) INFORMATION FOR SEQ ID NO:3:

### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387 base pairs

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153         (B) TYPE: nucleic acid
154         (C) STRANDEDNESS: single
155         (D) TOPOLOGY: linear
156
157     (ii) MOLECULE TYPE: DNA (genomic)
158
159     (vi) ORIGINAL SOURCE:
160         (A) ORGANISM: Monkey
161
162     (viii) POSITION IN GENOME:
163         (A) CHROMOSOME/SEGMENT: heavy variable domain of CE9.1
164
165     (ix) FEATURE:
166         (A) NAME/KEY: CDS
167         (B) LOCATION: 4..387
168
169     (ix) FEATURE:
170         (A) NAME/KEY: mat_peptide
171         (B) LOCATION: 61..387
172
173
174     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
175
176     ACC ATG GCC TGG GCT CTG CTG CTC CTC GGC CTC CTT GCT CAC TTT ACA      48
177     Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr
178     -19                -15                -10                -5
179
180     GAC TCT GCG GCC TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG      96
181     Asp Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val
182                1                5                10
183
184     TCC CCA GGA CAG ACG GCC GGG TTC ACC TGT GGG GGA GAC AAC GTT GGA      144
185     Ser Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly
186                15                20                25
187
188     AGG AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CAG GCC CCT GTG      192
189     Arg Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val
190                30                35                40
191
192     CTG GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA      240
193     Leu Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg
194     45                50                55                60
195
196     TTC TCT GGC TCC AAC TCA GGG AAC ACC GCC ACC CTG ACC ATC AGC GGG      288
197     Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
198                65                70                75
199
200     GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGT      336
201     Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser
202                80                85                90
203
204     ACT GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CGG CTG ACC GTC CTA      384
205     Thr Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu
  
```

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206          95          100          105
207
208      GGT
209      Gly
210
211
212
213      (2) INFORMATION FOR SEQ ID NO:4:
214
215          (i) SEQUENCE CHARACTERISTICS:
216              (A) LENGTH: 128 amino acids
217              (B) TYPE: amino acid
218              (D) TOPOLOGY: linear
219
220          (ii) MOLECULE TYPE: protein
221
222          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
223
224      Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp
225      -19          -15          -10          -5
226
227      Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser
228              1          5          10
229
230      Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg
231          15          20          25
232
233      Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu
234      30          35          40          45
235
236      Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe
237              50          55          60
238
239      Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val
240              65          70          75
241
242      Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr
243              80          85          90
244
245      Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly
246              95          100          105
247
248
249      (2) INFORMATION FOR SEQ ID NO:5:
250
251

```

(i) SEQUENCE CHARACTERISTICS:

252 (A) LENGTH: 702 base pairs  
253 (B) TYPE: nucleic acid  
254 (C) STRANDEDNESS: single  
255 (D) TOPOLOGY: linear

256

257 (ii) MOLECULE TYPE: DNA (genomic)

258

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION *US/09/612,914***

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Original Text